

## SEQUENCE LISTING

<110> GROSS, RICHARD W.  
DAVID J. MANCUSO

<120> CALCIUM INDEPENDENT PHOSPHOLIPASE A2 $\gamma$  POLYNUCLEOTIDES  
AND POLYPEPTIDES AND METHODS THEREFOR

<130> 15060-58

<140>

<141>

<150> 09/168,623

<151> 2000-07-18

<160> 104

<170> PatentIn Ver. 3.2

<210> 1

<211> 782

<212> PRT

<213> Homo sapiens

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Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His  
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 Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser  
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 Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln  
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 Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys  
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 385 390 395 400  
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 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly  
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 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp  
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 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val  
 645 650 655  
 Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr  
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 Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr  
 675 680 685  
 Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp  
 690 695 700  
 Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp  
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 Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys  
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 Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu  
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 atgattacct gaagtttaaat aagtaagacc atgaattatg gcatttctta aatgaagcgt 180  
 tcaagaagtg agagaatgtc atagaaaata aatgattttt aagttatgtc tattaatctg 240  
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 nttaaatgaa gcgttcaaga agtgagagaa tgtcatanaa aataaatgat ttttaagtta 180  
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274

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		1				5					10							
cga	gcg	agt	cgc	cgc	tgc	agc	cct	agt	gac	tgc	ggc	ctg	cat	ccc	gat	98		
Arg	Ala	Ser	Arg	Arg	Cys	Ser	Pro	Ser	Asp	Cys	Gly	Leu	His	Pro	Asp			
		15					20					25						
tgt	ctt	ctc	ctc	caa	ggc	cta	cat	gat	tac	ctg	aag	ttt	aat	aat	aat	146		
Cys	Leu	Leu	Leu	Gln	Gly	Leu	His	Asp	Tyr	Leu	Lys	Phe	Asn	Asn	Asn			
	30					35					40							
gca	aga	agt	gtt	tgt	ggg	aag	cag	aga	agc	aag	caa	ctg	tat	ttc	tt	193		
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atgattacct gaagttaa aagtaagacc atgaattatg gcattttcta aatgaagcgt 180
tcaagaagtg agagaatgtc atagaaaata aatgattttt aagtt atg tct att aat 237
                                         Met Ser Ile Asn
                                           1

ctg act gta gat ata tat att tac ctc ctt agt aat gca aga agt gtt      285
Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn Ala Arg Ser Val
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tgt ggg aag cag aga agc aag caa ctg tat ttc ttg ttc tca cct aag      333
Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu Phe Ser Pro Lys
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cat tac tgg agg ata agc cac atc agt cta caa aga ggt ttt cat aca 381  
 His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg Gly Phe His Thr  
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aac ata ata aga tgt aaa tgg acc aaa agt gaa gca cat tct tgc agt 429  
 Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala His Ser Cys Ser  
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aag cac tgt tac tct cca agc aac cat ggt tta cat att ggg att ttg 477  
 Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His Ile Gly Ile Leu  
 70 75 80

aaa ctt agc act tct gct ccc aag gga ctt aca aaa gtg aac att tgt 525  
 Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys Val Asn Ile Cys  
 85 90 95 100

atg tcc cgt att aaa agt act ttg aac tct gtt tca aag gct gtt ttt 573  
 Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala Val Phe  
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ggc aat caa aat gaa atg att tca cgt tta gct caa ttt aag cca agt 621  
 Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser  
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tcc caa att tta aga aaa gta tcg gat agt ggc tgg tta aaa cag aaa 669  
 Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys  
 135 140 145

aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat agt gac aaa tca 717  
 Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser  
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gca gaa aag agt cct ttt cca gaa gag aaa agt cac att ata gac aaa 765  
 Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys  
 165 170 175 180

gaa gaa gat ata ggt aaa cgc agt ctt ttt cat tac aca agt tct ata 813  
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acc aca aaa ttt gga gac tca ttc tac ttt tta tca aat cat att aat 861  
 Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn  
 200 205 210

tca tat ttc aaa cgt aag gaa aaa atg tct caa caa aag gaa aat gaa 909  
 Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu  
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cat ttc cgg gac aaa tca gaa ctt gaa gat aaa aag gta gaa gag ggg 957  
 His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly  
 230 235 240

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 Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser  
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gaa tct gta cat acg gtg gac aag cct aca agt cct tct gcg ata cct	1053
Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro	
265 270 275	
gat gtt ctt caa gtt tca act aaa caa agt att gct aac ttt ctt tct	1101
Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser	
280 285 290	
cgt ccc acg gaa ggt gta caa gct tta gta ggt ggt tat att ggt gga	1149
Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly	
295 300 305	
ctt gtc ccc aaa tta aag tat gat tca aag agt cag tca gaa gaa cag	1197
Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln	
310 315 320	
gaa gag cct gct aaa act gat cag gct gtc agc aaa gac aga aat gca	1245
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325 330 335 340	
gag gag aaa aag cgt tta tct ctt cag cga gaa aag att atc gca agg	1293
Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg	
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gtg agt att gat aac agg acc cgg gca tta gtt cag gca tta aga aga	1341
Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg	
360 365 370	
aca act gac cca aag ctc tgc att act agg gtt gaa gaa ctg act ttt	1389
Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe	
375 380 385	
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His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg	
390 395 400	
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Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu	
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cag gct gca gtt aga gaa att ttg gcc cta att ggc tat gtg gat cca	1533
Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro	
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Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr	
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Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr	
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Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr	
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ggt gcc ata tta gct ttc atg ttg ggg ttg ttt cat atg ccc ttg gat	1725
Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His Met Pro Leu Asp	
485 490 495 500	
gaa tgt gag gaa ctt tat cga aaa tta gga tca gat gta ttt tca caa	1773
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Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr	
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Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala	
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Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly	
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Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro	
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ggc tac ttt gca gaa tat gca ttg gga aat gat ctt cat caa gat gga	2109
Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly	
615 620 625	
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Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys	
630 635 640	
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Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr	
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Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu	
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Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu	
680 685 690	
gtc cat ata atg ctt gat ggc ctg tta cct cct gac acc tat ttt aga	2349
Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg	
695 700 705	



ttc aat cct gta atg tgt gaa aac ata cct cta gat gaa agt cga aat 2397  
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 710 715 720

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 Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg  
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aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta agt caa gaa aaa 2493  
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 745 750 755

aca act ctg cag aaa att aat gat tgg ata aaa tta aaa act gat atg 2541  
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 760 765 770

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gacattctct cacttcttga acgcttcatt taagaaatgc cataattcat ggtcttactt 180
attaaacttc aggtaatcat gtagaccttg gaggagaaga caatcgggat gcaggccgca 240
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gacattctct cacttcttga acgcttcatt taanaaatgc cataattcat ggtcttaccg 180
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gggctgcagc ggcgactcgc tcgttcccgg caatgacgtc cactccaacc ggctgcatc 180
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<220>
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38

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gca	aga	agt	gtt	tgt	ggg	aag	cag	aga	agc	aag	caa	ctg	tat	ttc	ttg	96
Ala	Arg	Ser	Val	Cys	Gly	Lys	Gln	Arg	Ser	Lys	Gln	Leu	Tyr	Phe	Leu	
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Phe	Ser	Pro	Lys	His	Tyr	Trp	Arg	Ile	Ser	His	Ile	Ser	Leu	Gln	Arg	
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ggc	ttt	cat	aca	aac	ata	ata	aga	tgt	aaa	tgg	acc	aaa	agt	gaa	gca	192
Gly	Phe	His	Thr	Asn	Ile	Ile	Arg	Cys	Lys	Trp	Thr	Lys	Ser	Glu	Ala	
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cat	tct	tgc	agt	aag	cac	tgt	tac	tct	cca	agc	aac	cat	ggc	tta	cat	240
His	Ser	Cys	Ser	Lys	His	Cys	Tyr	Ser	Pro	Ser	Asn	His	Gly	Leu	His	
	65				70				75				80			

att	ggg	att	ttg	aaa	ctt	agc	act	tct	gct	ccc	aag	gga	ctt	aca	aaa	288
Ile	Gly	Ile	Leu	Lys	Leu	Ser	Thr	Ser	Ala	Pro	Lys	Gly	Leu	Thr	Lys	
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Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser	
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Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln	
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ttt aag cca agt tcc caa att tta aga aaa gta tcg gat agt ggc tgg	432
Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp	
130 135 140	
tta aaa cag aaa aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat	480
Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr	
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Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His	
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Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr	
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Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser	
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Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys	
225 230 235 240	
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Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr	
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Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro	
260 265 270	
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Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala	
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Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys	
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Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln	
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Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys	
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Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly	
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Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp	
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His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met	
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His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val	
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Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr	
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Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp	
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Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys	
725 730 735	
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Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu	
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Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu	
755 760 765	

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 Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile  
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 Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn  
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 Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu  
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 His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly  
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 Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser  
                       145                      150                      155                      160  
 Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro  
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Arg	Pro	Thr	Glu	Gly	Val	Gln	Ala	Leu	Val	Gly	Gly	Tyr	Ile	Gly	Gly	195	200	205	
Leu	Val	Pro	Lys	Leu	Lys	Tyr	Asp	Ser	Lys	Ser	Gln	Ser	Glu	Glu	Gln	210	215	220	
Glu	Glu	Pro	Ala	Lys	Thr	Asp	Gln	Ala	Val	Ser	Lys	Asp	Arg	Asn	Ala	225	230	235	240
Glu	Glu	Lys	Lys	Arg	Leu	Ser	Leu	Gln	Arg	Glu	Lys	Ile	Ile	Ala	Arg	245	250	255	
Val	Ser	Ile	Asp	Asn	Arg	Thr	Arg	Ala	Leu	Val	Gln	Ala	Leu	Arg	Arg	260	265	270	
Thr	Thr	Asp	Pro	Lys	Leu	Cys	Ile	Thr	Arg	Val	Glu	Glu	Leu	Thr	Phe	275	280	285	
His	Leu	Leu	Glu	Phe	Pro	Glu	Gly	Lys	Gly	Val	Ala	Val	Lys	Glu	Arg	290	295	300	
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Gln	Ala	Ala	Val	Arg	Glu	Ile	Leu	Ala	Leu	Ile	Gly	Tyr	Val	Asp	Pro	325	330	335	
Val	Lys	Gly	Arg	Gly	Ile	Arg	Ile	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Thr	340	345	350	
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Glu	Cys	Glu	Glu	Leu	Tyr	Arg	Lys	Leu	Gly	Ser	Asp	Val	Phe	Ser	Gln	405	410	415	
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Cys	Leu	Trp	Pro	Asp	Val	Pro	Leu	Glu	Cys	Ile	Val	Ser	Leu	Gly	Thr	
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Asn	Glu	Gln	Lys	Met	Lys	Lys	Val	Ala	Lys	Ile	Leu	Ser	Gln	Glu	Lys	
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Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys	
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Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile	
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Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu	
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His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly	
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Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser	
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Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg	
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645 650 655	
aca act ctg cag aaa att aat gat tgg ata aaa tta aaa act gat atg	2016
Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met	
660 665 670	
tat gaa gga ctt cca ttc ttt tca aaa ttg tga	2049
Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu	
675 680	

&lt;210&gt; 17

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 17

tcaagtcgac atgatttcac gtttagc

27

&lt;210&gt; 18

&lt;211&gt; 661

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

Met	Ile	Ser	Arg	Leu	Ala	Gln	Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg
1				5					10					15	

Lys	Val	Ser	Asp	Ser	Gly	Trp	Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala
			20					25					30		

Ile	Lys	Ser	Leu	Lys	Lys	Tyr	Ser	Asp	Lys	Ser	Ala	Glu	Lys	Ser	Pro
	35						40					45			

Phe	Pro	Glu	Glu	Lys	Ser	His	Ile	Ile	Asp	Lys	Glu	Glu	Asp	Ile	Gly
	50					55					60				

Lys	Arg	Ser	Leu	Phe	His	Tyr	Thr	Ser	Ser	Ile	Thr	Thr	Lys	Phe	Gly
65					70					75					80

Asp	Ser	Phe	Tyr	Phe	Leu	Ser	Asn	His	Ile	Asn	Ser	Tyr	Phe	Lys	Arg
				85					90					95	

Lys	Glu	Lys	Met	Ser	Gln	Gln	Lys	Glu	Asn	Glu	His	Phe	Arg	Asp	Lys
			100					105					110		

Ser	Glu	Leu	Glu	Asp	Lys	Lys	Val	Glu	Glu	Gly	Lys	Leu	Arg	Ser	Pro
		115					120					125			

Asp	Pro	Gly	Ile	Leu	Ala	Tyr	Lys	Pro	Gly	Ser	Glu	Ser	Val	His	Thr
	130					135					140				

Val	Asp	Lys	Pro	Thr	Ser	Pro	Ser	Ala	Ile	Pro	Asp	Val	Leu	Gln	Val
145					150					155					160

Ser	Thr	Lys	Gln	Ser	Ile	Ala	Asn	Phe	Leu	Ser	Arg	Pro	Thr	Glu	Gly
			165						170					175	

Val	Gln	Ala	Leu	Val	Gly	Gly	Tyr	Ile	Gly	Gly	Leu	Val	Pro	Lys	Leu
			180					185					190		

Lys	Tyr	Asp	Ser	Lys	Ser	Gln	Ser	Glu	Glu	Gln	Glu	Glu	Pro	Ala	Lys
		195					200					205			

Thr	Asp	Gln	Ala	Val	Ser	Lys	Asp	Arg	Asn	Ala	Glu	Glu	Lys	Lys	Arg
	210					215					220				

Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn  
 225 230 235 240  
 Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys  
 245 250 255  
 Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe  
 260 265 270  
 Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu  
 275 280 285  
 Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg  
 290 295 300  
 Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly  
 305 310 315 320  
 Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala  
 325 330 335  
 Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His  
 340 345 350  
 Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala  
 355 360 365  
 Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu  
 370 375 380  
 Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly  
 385 390 395 400  
 Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp  
 405 410 415  
 Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr  
 420 425 430  
 Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val  
 435 440 445  
 Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His  
 450 455 460  
 Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met  
 465 470 475 480  
 Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu  
 485 490 495  
 Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn  
 500 505 510  
 Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp  
 515 520 525

Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser  
530 535 540

Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser  
545 550 555 560

Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu  
565 570 575

Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met  
580 585 590

Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln  
595 600 605

Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met  
610 615 620

Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys  
625 630 635 640

Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro  
645 650 655

Phe Phe Ser Lys Leu  
660

<210> 19  
<211> 1986  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(1983)

<400> 19  
atg att tca cgt tta gct caa ttt aag cca agt tcc caa att tta aga 48  
Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser Ser Gln Ile Leu Arg  
1 5 10 15

aaa gta tcg gat agt ggc tgg tta aaa cag aaa aac atc aaa caa gcc 96  
Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys Asn Ile Lys Gln Ala  
20 25 30

atc aaa tct ctg aaa aaa tat agt gac aaa tca gca gaa aag agt cct 144  
Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser Ala Glu Lys Ser Pro  
35 40 45

ttt cca gaa gag aaa agt cac att ata gac aaa gaa gaa gat ata ggt 192  
Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys Glu Glu Asp Ile Gly  
50 55 60

aaa cgc agt ctt ttt cat tac aca agt tct ata acc aca aaa ttt gga 240  
Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile Thr Thr Lys Phe Gly  
65 70 75 80

gac tca ttc tac ttt tta tca aat cat att aat tca tat ttc aaa cgt	288
Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn Ser Tyr Phe Lys Arg	
85 90 95	
aag gaa aaa atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa	336
Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys	
100 105 110	
tca gaa ctt gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca	384
Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro	
115 120 125	
gat cct ggc atc ctg gct tat aag cca ggc tca gaa tct gta cat acg	432
Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr	
130 135 140	
gtg gac aag cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt	480
Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val	
145 150 155 160	
tca act aaa caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt	528
Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly	
165 170 175	
gta caa gct tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta	576
Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu	
180 185 190	
aag tat gat tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa	624
Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys	
195 200 205	
act gat cag gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt	672
Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg	
210 215 220	
tta tct ctt cag cga gaa aag att atc gca agg gtg agt att gat aac	720
Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn	
225 230 235 240	
agg acc cgg gca tta gtt cag gca tta aga aga aca act gac cca aag	768
Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys	
245 250 255	
ctc tgc att act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt	816
Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe	
260 265 270	
cct gaa gga aaa gga gtg gct gtc aag gaa aga att att cca tat tta	864
Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu	
275 280 285	
tta cga ctg aga caa att aag gat gaa act ctt cag gct gca gtt aga	912
Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg	
290 295 300	



gaa att ttg gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly 305 310 315 320	960
atc cga att ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala 325 330 335	1008
ctc cag acc cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His 340 345 350	1056
cag ctc ttt gat tac att tgt ggt gta agc aca ggt gcc ata tta gct Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala 355 360 365	1104
ttc atg ttg ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu 370 375 380	1152
tat cga aaa tta gga tca gat gta ttt tca caa aat gtc att gtt gga Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly 385 390 395 400	1200
aca gta aaa atg agt tgg agc cat gca ttt tat gac agt caa aca tgg Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp 405 410 415	1248
gaa aac att ctt aag gat agg atg gga tct gca ctg atg att gaa aca Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr 420 425 430	1296
gca aga aac ccc aca tgt cct aag gta gct gct gta agt acc ata gta Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val 435 440 445	1344
aat aga ggg ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His 450 455 460	1392
ttt cct gga atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met 465 470 475 480	1440
tgg cag gcc att aga gcc tca tct gct gct cca ggc tac ttt gca gaa Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu 485 490 495	1488
tat gca ttg gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn 500 505 510	1536
aac cct tcg gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp 515 520 525	1584

gtg ccg tta gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt	1632
Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser	
530 535 540	
gat gtg aga aac acg gta aca tac aca agc ttg aaa act aaa ctt tct	1680
Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser	
545 550 555 560	
aat gtt atc aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt	1728
Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu	
565 570 575	
gat ggc ctg tta cct cct gac acc tat ttt aga ttc aat cct gta atg	1776
Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met	
580 585 590	
tgt gaa aac ata cct cta gat gaa agt cga aat gaa aag ctg gat cag	1824
Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln	
595 600 605	
ctg cag ttg gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg	1872
Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met	
610 615 620	
aaa aaa gtt gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa	1920
Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys	
625 630 635 640	
att aat gat tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca	1968
Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro	
645 650 655	
ttc ttt tca aaa ttg tga	1986
Phe Phe Ser Lys Leu	
660	

<210> 20  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 20  
 gtaagtcgac aatgtctcaa caaaagg

27

<210> 21  
 <211> 562  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu  
 1 5 10 15

Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly  
                   20                                  25                                  30  
 Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys  
                   35                                  40                                  45  
 Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys  
                   50                                  55                                  60  
 Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala  
                   65                                  70                                  75                                  80  
 Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp  
                                   85                                  90                                  95  
 Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln  
                                   100                                  105                                  110  
 Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu  
                   115                                  120                                  125  
 Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg  
                   130                                  135                                  140  
 Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile  
                   145                                  150                                  155                                  160  
 Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly  
                                   165                                  170                                  175  
 Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu  
                                   180                                  185                                  190  
 Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu  
                   195                                  200                                  205  
 Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile  
                   210                                  215                                  220  
 Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr  
                   225                                  230                                  235                                  240  
 Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe  
                                   245                                  250                                  255  
 Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu  
                   260                                  265                                  270  
 Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys  
                   275                                  280                                  285  
 Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys  
                   290                                  295                                  300  
 Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile  
                   305                                  310                                  315                                  320

[illegible]

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<210> 22
<211> 1689
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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&lt;222&gt; (1) .. (1686)

&lt;400&gt; 22

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Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu	
1 5 10 15	
gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca gat cct ggc	96
Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly	
20 25 30	
atc ctg gct tat aag cca ggc tca gaa tct gta cat acg gtg gac aag	144
Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys	
35 40 45	
cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt tca act aaa	192
Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys	
50 55 60	
caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt gta caa gct	240
Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala	
65 70 75 80	
tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta aag tat gat	288
Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp	
85 90 95	
tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa act gat cag	336
Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln	
100 105 110	
gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt tta tct ctt	384
Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu	
115 120 125	
cag cga gaa aag att atc gca agg gtg agt att gat aac agg acc cgg	432
Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg	
130 135 140	
gca tta gtt cag gca tta aga aga aca act gac cca aag ctc tgc att	480
Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile	
145 150 155 160	
act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt cct gaa gga	528
Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly	
165 170 175	
aaa gga gtg gct gtc aag gaa aga att att cca tat tta tta cga ctg	576
Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu	
180 185 190	
aga caa att aag gat gaa act ctt cag gct gca gtt aga gaa att ttg	624
Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu	
195 200 205	

gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga atc cga att Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile 210 215 220	672
ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct ctc cag acc Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr 225 230 235 240	720
cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat cag ctc ttt Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe 245 250 255	768
gat tac att tgt ggt gta agc aca ggt gcc ata tta gct ttc atg ttg Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu 260 265 270	816
ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt tat cga aaa Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys 275 280 285	864
tta gga tca gat gta ttt tca caa aat gtc att gtt gga aca gta aaa Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys 290 295 300	912
atg agt tgg agc cat gca ttt tat gac agt caa aca tgg gaa aac att Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile 305 310 315 320	960
ctt aag gat agg atg gga tct gca ctg atg att gaa aca gca aga aac Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn 325 330 335	1008
ccc aca tgt cct aag gta gct gct gta agt acc ata gta aat aga ggg Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly 340 345 350	1056
ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat ttt cct gga Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly 355 360 365	1104
atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg tgg cag gcc Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala 370 375 380	1152
att aga gcc tca tct gct gct cca ggc tac ttt gca gaa tat gca ttg Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu 385 390 395 400	1200
gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat aac cct tcg Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser 405 410 415	1248
gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat gtg ccg tta Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu 420 425 430	1296

gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt gat gtg aga	1344
Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg	
435 440 445	
aac acg gta aca tac aca agc ttg aaa act aaa ctt tct aat gtt atc	1392
Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile	
450 455 460	
aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt gat ggc ctg	1440
Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu	
465 470 475 480	
tta cct cct gac acc tat ttt aga ttc aat cct gta atg tgt gaa aac	1488
Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn	
485 490 495	
ata cct cta gat gaa agt cga aat gaa aag ctg gat cag ctg cag ttg	1536
Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu	
500 505 510	
gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg aaa aaa gtt	1584
Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val	
515 520 525	
gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa att aat gat	1632
Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp	
530 535 540	
tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca ttc ttt tca	1680
Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser	
545 550 555 560	
aaa ttg tga	1689
Lys Leu	

<210> 23  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 23	
gcatactcga gtcacaattt tgaaaagaat ggaagtcc	38

<210> 24  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 24  
gtacatacgg tggacaagcc ta 22

<210> 25  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 25  
cattcctctc cctttcactg gatccacata gcc 33

<210> 26  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 26  
Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln  
1 5 10 15

<210> 27  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
gaaaacctct ttgtagactg atgtggctta tcctccag 38

<210> 28  
<211> 5  
<212> PRT  
<213> Homo sapiens

<400> 28  
Ala Ser Cys Ser Val  
1 5

<210> 29  
<211> 302  
<212> DNA  
<213> Homo sapiens



<400> 29

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tcagcagggt cagaacctat aatttcattc ggtatattct gtatgggtga agatgtacag 60
ccagcaaaag ctttttaatt cgggaaaaca cgattggact tgcactttca aaagattacc 120
gtggttgcac agaagagact gactgggtca gaggttagtt acaggctgga aaaccagttt 180
agatgaaact gaagagcaag gatgaaagcc tgaactagag cagtggaaat gcgaatgtgg 240
agcagaggaa cgattcaaga aattctgctg taaaactcat cagacttcat gactgattaa 300
ag                                                                 302
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<210> 30

<211> 118

<212> DNA

<213> Homo sapiens

<400> 30

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ttttgccttt ctagagtgtt atacagctgg aatcatactg gtaggtctat ggtccgaatg 60
tttgtgcttc tcaaaattca tgtggaaatc ataaccgcta aagtgatggt attaagag 118
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<210> 31

<211> 92

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 31

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tgtttgatgt ttttctgttt taaccagcca ctatccgata cttttcttaa aatttgggaa 60
cttggtctaa attgagctaa acgtgaaatc at                                                                 92
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<210> 32

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 32

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tcgacctgat ttcacgttta gctcaatt                                                                 28
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<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 33  
tcgactaagc caagttccca aattttaa 28

<210> 34  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 34  
tcgacgaaaa gtatcggata gtggctgg 28

<210> 35  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 35  
tcgacttaaa acagaaaaac atcaaaca 28

<210> 36  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 36  
ggactaaagt gcaaatcgag ttaaccgg 28

<210> 37  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 37  
gattcggttc aagggtttaa aattccgg 28

<210> 38  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 38  
 gcttttcata gcctatcacc gaccccg 28

<210> 39  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 39  
 gaattttgtc tttttgtagt ttgtccg 28

<210> 40  
 <211> 353  
 <212> PRT  
 <213> Mus sp.

<400> 40  
 Met Ser Ile Asn Leu Thr Leu Asp Ile Tyr Ile Tyr Phe Leu Asn Asn  
 1 5 10 15  
 Ala Arg Ser Leu Cys Gly Lys Gln Arg Ser Lys Gln Leu His Phe Val  
 20 25 30  
 Cys Ser Lys Gln Tyr Trp Arg Met Asn His Val Asn Val His Arg Glu  
 35 40 45  
 Phe His Thr Ser Lys Lys Ser Cys Lys Trp Asn Arg Ser Glu Ala His  
 50 55 60  
 Cys Ser Lys His Trp His Ser Pro Ser Asn His Gly Leu His Phe Gly  
 65 70 75 80  
 Ile Val Arg Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys Val Ser  
 85 90 95  
 Ile His Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala  
 100 105 110  
 Ile Phe Gly Ser Gln Asn Glu Met Val Thr Arg Leu Ala Gln Phe Lys  
 115 120 125

Pro Ser Ser Arg Ile Leu Arg Lys Val Ser Asp Lys Gly Trp Leu Lys  
 130 135 140  
 Gln Lys Asn Val Lys Gln Ala Val Glu Ser Leu Lys Asn Tyr Ser Asp  
 145 150 155 160  
 Lys Ser Ala Gly Lys Asn Ser Leu Ala Glu Gln Lys Ser Tyr Phe Ala  
 165 170 175  
 Asp Lys Glu Glu Asp Ser Gly Lys His Ser Leu Phe His Tyr Thr Tyr  
 180 185 190  
 Gly Ile Thr Thr Arg Phe Gly Glu Ser Phe Ser Val Leu Ala Asn His  
 195 200 205  
 Ile Asn Ser Tyr Phe Lys Ser Lys Gly Lys Met Ser Gln Thr Lys Glu  
 210 215 220  
 Asp Lys Gln Leu Gln Asp Lys Pro Asp Leu Glu Glu Arg Lys Ser Ser  
 225 230 235 240  
 Ser Pro Gly Pro Asp Thr Val Ala Asp Arg Pro Asp Ser Glu Ser Pro  
 245 250 255  
 Leu Glu Val Lys Asp Lys Leu Ser Ser Pro Thr Gln Met Pro Glu Ala  
 260 265 270  
 His Pro Val Ser Ala Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro  
 275 280 285  
 Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val  
 290 295 300  
 Pro Lys Leu Lys Ser Asp Pro Lys Ser Pro Pro Glu Glu Gln Glu Val  
 305 310 315 320  
 Ser Ala Lys Thr Glu Gln Ala Val Asx Lys Asp Lys Lys Ala Glu Glu  
 325 330 335  
 Lys Lys Arg Val Leu Leu Gln Gln Glu Lys Ile Ile Ala Arg Val Ser  
 340 345 350  
 Ile

<210> 41  
 <211> 353  
 <212> PRT  
 <213> Rattus sp.

<400> 41  
 Met Ser Ile Asn Leu Ile Leu Asp Ile Tyr Ile Tyr Phe Leu Asn Asn  
 1 5 10 15  
 Ala Arg Ser Phe Cys Gly Lys Gln Arg Ser Lys Gln Leu Asn Phe Leu  
 20 25 30

Cys Ser Lys Gln Tyr Trp Arg Met Asn His Val Asn Val His Arg Glu  
 35 40 45  
 Phe His Thr Ser Lys Lys Ser Cys Lys Trp Asn Arg Ser Glu Ala His  
 50 55 60  
 Cys Ser Lys His Trp His Ser Ser Ser Asn His Gly Val His Ile Gly  
 65 70 75 80  
 Ile Val Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys Val Ser  
 85 90 95  
 Ile His Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala  
 100 105 110  
 Ile Phe Gly Ser Gln Asn Glu Met Val Ser Arg Leu Ala Gln Phe Lys  
 115 120 125  
 Pro Ser Ser Arg Ile Phe Arg Lys Val Ser Asp Arg Gly Trp Leu Lys  
 130 135 140  
 His Lys Asn Val Lys Gln Ala Ile Glu Ser Leu Lys Asn Tyr Ser Asp  
 145 150 155 160  
 Lys Ser Ala Glu Lys Asn Ser Phe Ala Glu Gln Lys Ser Tyr Phe Ala  
 165 170 175  
 Asp Lys Glu Glu Gly Ser Asp Lys His Ser Leu Tyr His Tyr Ala Tyr  
 180 185 190  
 Arg Ile Thr Thr Arg Phe Gly Glu Ser Phe Tyr Phe Leu Ala Asn His  
 195 200 205  
 Ile Asn Ser Tyr Phe Lys Asn Lys Glu Lys Met Ser Gln Thr Lys Glu  
 210 215 220  
 Asp Arg Gln Leu Gln Asp Lys Pro Cys Leu Glu Glu Ser Lys Ser Ile  
 225 230 235 240  
 Ser Pro Ser Pro Asp Ile Leu Thr Asp Arg Pro Asp Ser Gly Pro Pro  
 245 250 255  
 Leu Asn Val Glu Asp Lys Leu Ser Ser Ser Thr Gln Leu Pro Glu Ala  
 260 265 270  
 Leu Pro Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro  
 275 280 285  
 Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val  
 290 295 300  
 Pro Lys Leu Lys Ser Asp Pro Lys Ser Gln Pro Glu Glu Glu Glu Glu  
 305 310 315 320  
 Pro Ser Lys Thr Asp Glu Pro Ile Cys Lys Asp Lys Lys Ala Glu Glu  
 325 330 335

Lys Lys Arg Val Leu Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser  
                   340                  345                  350

Ile

<210> 42

<211> 359

<212> PRT

<213> Homo sapiens

<400> 42

Met Ser Ile Asn Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn  
   1                  5                  10                  15

Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu  
                   20                  25                  30

Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg  
           35                  40                  45

Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala  
   50                  55                  60

His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His  
   65                  70                  75                  80

Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys  
                   85                  90                  95

Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser  
                   100                  105                  110

Lys Ala Val Phe Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln  
   115                  120                  125

Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp  
   130                  135                  140

Leu Lys Gln Lys Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr  
   145                  150                  155                  160

Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His  
                   165                  170                  175

Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr  
   180                  185                  190

Thr Ser Ser Ile Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser  
   195                  200                  205

Asn His Ile Asn Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln  
   210                  215                  220

Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys  
 225 230 235 240  
 Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr  
 245 250 255  
 Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro  
 260 265 270  
 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala  
 275 280 285  
 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly  
 290 295 300  
 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln  
 305 310 315 320  
 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys  
 325 330 335  
 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys  
 340 345 350  
 Ile Ile Ala Arg Val Ser Ile  
 355

<210> 43  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(12)

<400> 43  
 cag cga gaa aag gcaagtt  
 Gln Arg Glu Lys  
 1

19

<210> 44  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Gln Arg Glu Lys  
 1

<210> 45  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(18)

<400> 45  
 att atc gca agg gtg agt  
 ile ile ala arg val ser  
 1 5

18

<210> 46  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 ile ile ala arg val ser  
 1 5

<210> 47  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(20)

<400> 47  
 gaa aag gca agt tgt tca gt gtgctt  
 glu lys ala ser cys ser val  
 1 5

26

<210> 48  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 glu lys ala ser cys ser val  
 1 5

<210> 49  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Illustrative  
 conserved lipase motif

<220>  
 <221> MOD\_RES



<222> (2)  
 <223> Variable amino acid

<400> 49  
 Gly Xaa Ser Gly Ser  
     1                    5

<210> 50  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Illustrative  
         conserved motif

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Variable amino acid

<400> 50  
 Gly Xaa Ser Thr Gly  
     1                    5

<210> 51  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Ile Ile Ala Arg  
     1

<210> 52  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Ile Cys Gly Val Ser Thr Gly  
     1                    5

<210> 53  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 53  
 Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly  
     1                    5                    10

<210> 54  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: 6-His tag

<400> 54  
 His His His His His His  
 1 5

<210> 55  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 55  
 aaaagtcgac atgaagccat caaatctc 28

<210> 56  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 56  
 aagagtcgac atgaggtaaa cgcagtc 27

<210> 57  
 <211> 315  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 atgtctatta atctgactgt agatatatat atttacctcc ttagtaatgc aagaagtgtt 60  
 tgtgggaagc agagaagcaa gcaactgtat ttcttggtct cacctaagca ttactggagg 120  
 ataagccaca tcagtctaca aagaggtttt catacaaaca taataagatg taaatggacc 180  
 aaaagtgaag cacattcttg cagtaagcac tggtactctc caagcaacca tggtttacat 240  
 attgggattt tgaaacttag cacttctgct cccaagggac ttacaaaagt gaacatttgt 300  
 atgtcccgtg ttaaa 315

<210> 58  
 <211> 19  
 <212> PRT  
 <213> Homo sapiens

<400> 58

Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser Ser Gln Ile Leu Arg  
 1 5 10 15

Lys Val Ser

<210> 59

<211> 45

<212> DNA

<213> Homo sapiens

<400> 59

tattaatctg actgtagata tatatatatta cctccttagt aatgc 45

<210> 60

<211> 6

<212> DNA

<213> Homo sapiens

<400> 60

caagtg 6

<210> 61

<211> 6

<212> DNA

<213> Homo sapiens

<400> 61

caggtg 6

<210> 62

<211> 6

<212> DNA

<213> Homo sapiens

<400> 62

caggtg 6

<210> 63

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 63

gttgaagctt gtgtctatta atctgactgt a 31

<210> 64  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 64  
 tagaccatgg tggcttatcc tccagtaatg c 31

<210> 65  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 65  
 gtgtaagctt gaagcagaga agcaagcaac tg 32

<210> 66  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 66  
 actgccatgg tggccttcac ttttggtcca tttac 35

<210> 67  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 67  
 tggaaagctt gccacatcag tctacaaag 29

<210> 68  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 68  
 tgctccatgg tggcatccca atatgtaaac ca 32

<210> 69  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 69  
 gaaccaagct tgaagcacat tcttgcaagta agca 34

<210> 70  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 70  
 caaaacatgt tggctacggg acatacaaatt gttca 35

<210> 71  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 71  
 gttgaagctt tttgaaactt agcacttctg c 31

<210> 72  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 72  
 attccatggg ggctgaaatc atttcatttt gattgcc 37

<210> 73  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 73  
 tcaaaagctt atgatttcac gtttagctc 29  
  
 <210> 74  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 74  
 ctttccatgg tggctgtcac tatatttttt ca 32  
  
 <210> 75  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 75  
 gattaaaggt atggtggt 18  
  
 <210> 76  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 76  
 acctccttag taatgcaag 19  
  
 <210> 77  
 <211> 22  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 77  
 gcgtcacttc cgctgggggc gg 22  
  
 <210> 78  
 <211> 11  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 78  
 gccagtgttt g 11  
  
 <210> 79  
 <211> 13

<212> DNA  
 <213> Homo sapiens

<400> 79  
 ttttaagtta tgt 13

<210> 80  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens

<400> 80  
 aacatttgta tgt 13

<210> 81  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
 caaaatgaaa tga 13

<210> 82  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
 aaggaaaaaa tgt 13

<210> 83  
 <211> 13  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Consensus  
 sequence

<400> 83  
 gccgccrcca tgg 13

<210> 84  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

<400> 84  
 attataatac tgtgcagcaa gggcaataag agaagtgagc acaggtggaa ggaatgattc 60  
 attctatgag tagtgaggta agattttcct ggctgaagga caaacaatc tttaggagga 120  
 caaggtggaa ggggagctaa gccaacagca tgaccaaggc actaagtatg aaaaggaaca 180  
 agagtatctg gggaagtaca ggtgtggctg gaggatagag agtgagaggc aagtggtgaa 240

agtaaaggct ggaaggctcag cagggtcaga 270

<210> 85  
 <211> 11  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 ggacaggtgg g 11

<210> 86  
 <211> 11  
 <212> DNA  
 <213> Homo sapiens

<400> 86  
 cacaggtggt g 11

<210> 87  
 <211> 12  
 <212> DNA  
 <213> Homo sapiens

<400> 87  
 cgacaggtgg tg 12

<210> 88  
 <211> 64  
 <212> DNA  
 <213> Mus sp.

<400> 88  
 gcgtcacttc cgctgggggc ggggcgtagc ggtgggtggt gctggtcacg ccagtgtttg 60  
 ggg 64

<210> 89  
 <211> 63  
 <212> DNA  
 <213> Rattus sp.

<400> 89  
 gcgtcacttc cgctgggggc ggggcgtagc ggaggggtgag gctgtagcgc cagtgtttgg 60  
 ggt 63

<210> 90  
 <211> 76  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
 gcgtcacttc cgctgggggc ggagcggggc ggggctgagt ggggtggcgac ctagctgctg 60



cgccagtgtt tgtgtt 76

<210> 91  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
 gcatcccggt aagtagcc 18

<210> 92  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
 acctccttag taatgcaag 19

<210> 93  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 93  
 gtggccgggt ggtccacctc gg 22

<210> 94  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 94  
 ttgatagtta tctattacag tcttcttaga ttgaaacaa 39

<210> 95  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 95  
 Leu Arg Lys Val Ser  
 1 5

<210> 96  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 96  
 Gly Gly Gly Thr Arg Gly  
           1                  5

<210> 97  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
 Gly Val Ser Thr Gly  
           1                  5

<210> 98  
 <211> 11  
 <212> DNA  
 <213> Homo sapiens

<400> 98  
 tctcacctaa g

11

<210> 99  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 99  
 Asn His Gly Leu Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala  
       1                  5                  10

<210> 100  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 100  
 Lys Val Asn Ile Cys Met  
       1                  5

<210> 101  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 101  
 Asn Gln Asn Glu Met Ile  
       1                  5

<210> 102  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 102  
Ile Ser Arg Leu  
1

<210> 103  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 103  
Ile Gly Lys Arg  
1

<210> 104  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 104  
tattaatctg actgtagata tatatatatta cctccttagt aatgc

45